

IN THE CLAIMS

Amend the claims as follows.

1. (Currently Amended) A method of producing a complex mixture of cDNA comprising reverse transcribing mRNA from tissues or cells, said reverse transcribing comprising adding, in a mRNA reaction medium, elongation terminators, said producing further comprising recovering said complex cDNA mixture formed from said reverse transcribing, said complex cDNA mixture representing the number and level of expression of genes extracted from said tissues or cells.

2. (Original) A method according to Claim 1, characterized by the use of dideoxynucleotides as elongation terminators.

Claim 3. (Canceled)

4. (Previously Presented) cDNA mixtures as obtained by application of the method according to Claim 1.

Claim 5 (Canceled).

6. (Currently Amended) A method for studying the profiles of expression of the genes present in a tissue or in cells, characterized in that it comprises contacting cDNA

mixtures according to Claim 4 with DNA corresponding to gene sequences of said tissue.

7. (Currently Amended) A method for detecting or a method for identifying a tissue-specific DNA sequence comprising hybridizing a complex cDNA mixture of claim 4 to ~~tissue~~-DNA corresponding to gene sequences of said tissue wherein isolated DNA from said tissue is bound to a filter, said hybridization being conducted under conditions which allow said cDNA mixtures to hybridize to said DNA corresponding to gene sequences of said tissue, and detecting hybridization of cDNA from said mixture to said ~~tissue~~-DNA corresponding to gene sequences of said tissue such that said hybridization indicates or identifies said tissue-specific DNA.